AMENDMENTS TO THE SPECIFICATION:

Please insert the following Brief Description of the Drawings at page 9 of the specification, between lines 15 and 16.

-- BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 2 shows the binding of ^{125}I-labeled Bt3 toxins to *M. sexta* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 3 shows the binding of ^{125}I-labeled Bt73 toxins to M. sexta brush border membrane vesicles as a function of the concentration of competitor.

FIG. 4 shows the binding of ^{125}I-labeled Bt2 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 5 shows the binding of ^{125}I-labeled Bt3 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 6 shows the binding of ^{125}I-labeled Bt73 toxins to *H. virescens* brush border membrane vesicles as a function of the concentration of competitor.

FIG. 7 shows the binding of ^{125}I-labeled Bt2 toxins to *P. brassicae* brush border membrane vesicles.

FIG. 8 shows the binding of ^{125}I-labeled Bt14 toxins to *P. brassicae* brush border membrane vesicles.

FIG. 9 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles.

FIG. 10 shows the binding of ^{125}I-labeled Bt15 toxins to *M. sexta* brush border membrane vesicles.

FIG. 11 shows the binding of ^{125}I-labeled Bt2 toxins to *M. sexta* brush border membrane vesicles

FIG. 12 shows the binding of ^{125}I-labeled Bt18 toxins to *M. sexta* brush border membrane vesicles.

FIG. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame of the *bt4* gene, isolated from HD-68 (SEQ ID NO: 5).

FIG. 14 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame of the *bt15* gene, isolated from HD-110 (SEQ ID NO: 7).

FIGS. 15A-15C schematically show (a) the construction of pVE29; (b) the construction of pVE35; and (c) the construction of pTHW88.

FIGS. 16A-16E schematically show (a) the construction of pHW44; (b) the construction of pHW67; (c) the construction of pHW71; (d) the construction of pTHW94; and (e) restriction map of the pTHW94 vector.

FIG. 17 schematically shows the construction of a hybrid *bt2-bt* gene with a C-terminal *bt2* gene fragment (bt860) encoding the toxic core of the Bt2 protoxin in frame with a C-terminal truncated bt14 gene fragment encoding the toxic core of the Bt14 protoxin.

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Please replace the paragraph beginning on Page 26, line 15 and ending on Page 26, line 30 with the following:

bt4

gene: A genomic library was prepared from total DNA of strain *B. thuringiensis aizawai* HD-68. Using the 1.1 kb internal HindIII fragment of the bt2 gene as a probe, a gene designated bt4 was isolated. Characterization of this gene revealed an open reading frame of 3495 bp which encodes a protoxin of 132 kDa and a trypsin activated toxin fragment of 60 kDa. This (insect controlling protein) gene differs from previously identified genes and was also found in several other strains of subspecies *aizawai* and *entomocidus* including HD-110. FIG. 13 shows the nucleotide sequence and deduced amino acid sequence of the open reading frame ("ORF") of the *bt4* gene (SEQ ID NO: 5) extending from nucleotide 264 to nucleotide 3761.

Please replace the paragraph beginning on Page 27, line 9 and ending on Page 28, line 2 with the following:

The second gene was called "*bt15*". FIG. 14 shows the nucleotide sequence and deduced amino acid sequence of the ORF of the *bt15* gene (SEQ ID NO: 7), isolated from HD-110, extending from nucleotide 234 to nucleotide 3803. The Shine and Dalgarno sequence, preceding the initiation codon is underlined. This gene has an open reading frame of 3567 bp which encodes a protoxin of 135 kDa and a 63 kDa toxin fragment. A similar gene has been described by Honee et al. 1988, isolated from *B. thuringiensis entomocidus* 60.5. The bt15 gene differs from the published sequence at three positions: an Ala codon (GCA) is present instead of an Arg codon (CGA) at position 925 and a consecution of a Thr-His codon (ACGCAT) is present instead of a Thr-Asp codon (ACCGAT) at position 1400. (The numbers of the positions are according to Honnee et al., 1988). Another similar gene has been described in EP 0295156, isolated from *B. thuringiensis aizawai* 7-29 and *entomocidus* 6-01. The *bt15* gene is different from this published nucleotide sequence at three different places: 1) a Glu codon (GAA) instead of an Ala codon (GCA) at (position. 700; 2) the sequence (SEQ ID NO:1) TGG, CCA, GCG, CCA instead of (SEQ ID NO:2) TGC, CAG, CGC, CAC, CAT at position 1456 and 3) an Arg codon (CGT) instead of an Ala codon (GCG) at position 2654. (The numbers of the positions are according to EP 0295156).

Please replace the paragraph beginning on page 29, line 10 and ending on page 29, line 18 with the following amended paragraph:

In the case of the *bt15* gene, the conversion of the TT nucleotides, immediately in front of the ATG codon, into CC yielded a NcoI site overlapping with the ATG initiation codon. This site was introduced using the pMa/c vectors for site-directed mutagenesis (Stanssens et al., 1987) and a 28-mer oligonucleotide with the following sequence (SEQ ID NO: 3): 5'-CGGAGGTATTCCATGGAGGAAAATAATC-3'.

Please replace the paragraph beginning on page 29, line 22 and ending on page 29, line 27 with the following amended paragraph:

According to Brizzard and Whiteley (1988), the initiation codon of the *bt14* gene is a TTG codon. Thus, a NcoI site was created in a like manner at this codon for site directed mutagenesis using a 34-mer oligonucleotide with the following sequence (SEQ ID NO: 4): 5'-CCTATTTGAAGCCATGGTAACTCCTCCTTTTATG-3'.